



SEQUENCE LISTING

<110> Combadiere et al.

<120> CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS AND THERAPEUTIC AGENTS FOR HIV INFECTION

<130> 66645-01

<140> US 10/700,313

<141> 2003-10-31

<150> US 60/018,508

<151> 1996-05-28

<150> 08/864,458

<151> 1997-05-28

<160> 10

<170> PatentIn version 3.3

<210> 1

<211> 1225

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (27)..(1082)

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Met Asp Tyr Gln Val Ser Ser Pro Ile
1 5

53

tat gac atc aat tat tat aca tcg gag ccc tgc caa aaa atc aat gtg
Tyr Asp Ile Asn Tyr Tyr Ser Glu Pro Cys Gln Lys Ile Asn Val
10 15 20 25

101

aag caa atc gca gcc cgc ctc ctg cct ccg ctc tac tca ctg gtg ttc
Lys Gln Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe
30 35 40

149

atc ttt ggt ttt gtg ggc aac atg ctg gtc atc ctc atc ctg ata aac
Ile Phe Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn
45 50 55

197

tgc aaa agg ctg aag agc atg act gac atc tac ctg ctc aac ctg gcc
Cys Lys Arg Leu Lys Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala
60 65 70

245

atc tct gac ctg ttt ttc ctt act gtc ccc ttc tgg gct cac tac
Ile Ser Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr
75 80 85

293

ttg gcc gcc cag tgg gac ttt gga aat aca atg tgt caa ctc ttg aca Leu Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu Leu Thr 90 95 100 105	341
ggg ctc tat ttt ata ggc ttc ttc tct gga atc ttc atc atc ctc Gly Leu Tyr Phe Ile Gly Phe Ser Gly Ile Phe Phe Ile Ile Leu 110 115 120	389
ctg aca atc gat agg tac ctg gct gtc gtc cat gct gtg ttt gct tta Leu Thr Ile Asp Arg Tyr Leu Ala Val Val His Ala Val Phe Ala Leu 125 130 135	437
aaa gcc agg acg gtc acc ttt ggg gtg gtg aca agt gtg atc act tgg Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp 140 145 150	485
gtg gtg gct gtg ttt gcg tct ctc cca gga atc atc ttt acc aga tct Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser 155 160 165	533
caa aaa gaa ggt ctt cat tac acc tgc agc tct cat ttt cca tac agt Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe Pro Tyr Ser 170 175 180 185	581
cag tat caa ttc tgg aag aat ttc cag aca tta aag ata gtc atc ttg Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu 190 195 200	629
ggg ctg gtc ctg ccg ctg ctt gtc atg gtc atc tgc tac tcg gga atc Gly Leu Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile 205 210 215	677
cta aaa act ctg ctt cgg tgt cga aat gag aag aag agg cac agg gct Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala 220 225 230	725
gtg agg ctt atc ttc acc atc atg att gtt tat ttt ctc ttc tgg gct Val Arg Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala 235 240 245	773
ccc tac aac att gtc ctt ctc ctg aac acc ttc cag gaa ttc ttt ggc Pro Tyr Asn Ile Val Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly 250 255 260 265	821
ctg aat aat tgc agt agc tct aac agg ttg gac caa gct atg cag gtg Leu Asn Asn Cys Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val 270 275 280	869
aca gag act ctt ggg atg acg cac tgc tgc atc aac ccc atc atc tat Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr 285 290 295	917
gcc ttt gtc ggg gag aag ttc aga aac tac ctc tta gtc ttc ttc caa Ala Phe Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln 300 305 310	965
aag cac att gcc aaa cgc ttc tgc aaa tgc tgt tct att ttc cag caa	1013

Lys His Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln				
315	320	325		
gag gct ccc gag cga gca agc tca gtt tac acc cga tcc act ggg gag				1061
Glu Ala Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu				
330	335	340	345	
cag gaa ata tct gtg ggc ttg tgacacggac tcaagtggc tggtgaccca				1112
Gln Glu Ile Ser Val Gly Leu				
350				
gtcagagttg tgcacatggc ttagtttca tacacagcct gggctggggg tgggtggga				1172
gaggtctttt ttaaaaggaa gttactgtta tagagggtct aagattcatc cat				1225
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Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn				
35	40	45		
Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met				
50	55	60		
Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu				
65	70	75	80	
Leu Thr Val Pro Phe Trp Ala His Tyr Leu Ala Ala Gln Trp Asp Phe				
85	90	95		
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe				
100	105	110		
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu				
115	120	125		
Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe				
130	135	140		

Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
145 150 155 160

Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
165 170 175

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
180 185 190

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
195 200 205

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
210 215 220

Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
225 230 235 240

Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
245 250 255

Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
260 265 270

Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
275 280 285

His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
290 295 300

Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
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Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
325 330 335

Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
340 345 350

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<211> 1225
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (27) .. (1082)

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aagaaaactct ccccggtgg aacaag atg gat tat caa gtg tca agt cca atc
Met Asp Tyr Gln Val Ser Ser Pro Ile
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53

tat gac atc aat tat tat aca tcg gag ccc tgc caa aaa atc aat gtg
Tyr Asp Ile Asn Tyr Tyr Ser Glu Pro Cys Gln Lys Ile Asn Val
10 15 20 25

101

aag caa atc gca gcc cgcc ctc ctg cct ccg ctc tac tca ctg gtg ttc
Lys Gln Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe
30 35 40

149

atc ttt ggt ttt gtg ggc aac atg ctg gtc atc ctc atc ctg ata aac
Ile Phe Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn
45 50 55

197

tgc aaa agg ctg aag agc atg act gac atc tac ctg ctc aac ctg gcc
Cys Lys Arg Leu Lys Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala
60 65 70

245

atc tct gac ctg ttt ttc ctt act gtc ccc ttc tgg gct cac tat
Ile Ser Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr
75 80 85

293

gct gcc gcc cag tgg gac ttt gga aat aca atg tgt caa ctc ttg aca
Ala Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu Leu Thr
90 95 100 105

341

ggg ctc tat ttt ata ggc ttc ttc tct gga atc ttc ttc atc atc ctc
Gly Leu Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Leu
110 115 120

389

ctg aca atc gat agg tac ctg gct gtc gtc cat gct gtg ttt gct tta
Leu Thr Ile Asp Arg Tyr Leu Ala Val Val His Ala Val Phe Ala Leu
125 130 135

437

aaa gcc agg acg gtc acc ttt ggg gtg gtg aca agt gtg atc act tgg
Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp
140 145 150

485

gtg gtg gct gtg ttt gcg tct ctc cca gga atc atc ttt acc aga tct
Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser
155 160 165

533

caa aaa gaa ggt ctt cat tac acc tgc agc tct cat ttt cca tac agt
Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe Pro Tyr Ser
170 175 180 185

581

cag tat caa ttc tgg aag aat ttc cag aca tta aag ata gtc atc ttg

629

Gln	Tyr	Gln	Phe	Trp	Lys	Asn	Phe	Gln	Thr	Leu	Lys	Ile	Val	Ile	Leu		
190								195					200				
ggg	ctg	gtc	ctg	ccg	ctg	ctt	gtc	atg	gtc	atc	tgc	tac	tcg	gga	atc		677
Gly	Leu	Val	Leu	Pro	Leu	Leu	Val	Met	Val	Ile	Cys	Tyr	Ser	Gly	Ile		
205								210					215				
cta	aaa	act	ctg	ctt	cg	tgt	cga	aat	gag	aag	aag	agg	cac	agg	gct		725
Leu	Lys	Thr	Leu	Leu	Arg	Cys	Arg	Asn	Glu	Lys	Lys	Arg	His	Arg	Ala		
220								225					230				
gtg	agg	ctt	atc	tcc	acc	atc	atg	att	gtt	tat	ttt	ctc	tcc	tgg	gct		773
Val	Arg	Leu	Ile	Phe	Thr	Ile	Met	Ile	Val	Tyr	Phe	Leu	Phe	Trp	Ala		
235								240					245				
ccc	tac	aac	att	gtc	ctt	ctc	ctg	aac	acc	tcc	cag	gaa	ttc	ttt	ggc		821
Pro	Tyr	Asn	Ile	Val	Leu	Leu	Leu	Asn	Thr	Phe	Gln	Glu	Phe	Phe	Gly		
250								255					260				265
ctg	aat	aat	tgc	agt	agc	tct	aac	agg	ttg	gac	caa	gct	atg	cag	gtg		869
Leu	Asn	Asn	Cys	Ser	Ser	Asn	Arg	Leu	Asp	Gln	Ala	Met	Gln	Val			
270								275					280				
aca	gag	act	ctt	ggg	atg	acg	cac	tgc	tgc	atc	aac	ccc	atc	atc	tat		917
Thr	Glu	Thr	Leu	Gly	Met	Thr	His	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr		
285								290					295				
gcc	ttt	gtc	ggg	gag	aag	ttc	aga	aac	tac	ctc	tta	gtc	ttc	ttc	caa		965
Ala	Phe	Val	Gly	Glu	Lys	Phe	Arg	Asn	Tyr	Leu	Leu	Val	Phe	Phe	Gln		
300								305					310				
aag	cac	att	gcc	aaa	cgc	ttc	tgc	aaa	tgc	tgt	tct	att	ttc	cag	caa		1013
Lys	His	Ile	Ala	Lys	Arg	Phe	Cys	Lys	Cys	Cys	Ser	Ile	Phe	Gln	Gln		
315								320					325				
gag	gct	ccc	gag	cga	gca	agc	tca	gtt	tac	acc	cga	tcc	act	ggg	gag		1061
Glu	Ala	Pro	Glu	Arg	Ala	Ser	Ser	Val	Tyr	Thr	Arg	Ser	Thr	Gly	Glu		
330								335					340				345
cag	gaa	ata	tct	gtg	ggc	ttg	tgacacggac	tcaagtgggc	tggtgaccca								1112
Gln	Glu	Ile	Ser	Val	Gly	Leu											
350																	
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Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
35 40 45

Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
50 55 60

Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
65 70 75 80

Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
85 90 95

Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
100 105 110

Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
115 120 125

Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
130 135 140

Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
145 150 155 160

Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
165 170 175

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
180 185 190

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
195 200 205

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
210 215 220

Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
225 230 235 240

Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
245 250 255

Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
260 265 270

Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
275 280 285

His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
290 295 300

Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
305 310 315 320

Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
325 330 335

Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
340 345 350

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Tyr Ser Gln Tyr Gln Phe Trp Lys
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His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
35 40 45

Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
50 55 60

Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
65 70 75 80

Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro
85 90 95

Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
100 105 110

Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile
115 120 125

Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
130 135 140

Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
145 150 155 160

Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
165 170 175

Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
180 185 190

Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
195 200 205

Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
210 215 220

Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
225 230 235 240

Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
245 250 255

Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
260 265 270

Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
275 280 285

Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
290 295 300

Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg Tyr Leu Ser Val Phe Phe
305 310 315 320

Arg Lys His Ile Thr Lys Arg Phe Cys Lys Gln Cys Pro Val Phe Tyr
325 330 335

Arg Glu Thr Val Asp Gly Val Thr Ser Thr Asn Thr Pro Ser Thr Gly
340 345 350

Glu Gln Glu Val Ser Ala Gly Leu
355 360

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Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe
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Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly
35 40 45

Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg
50 55 60

Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
65 70 75 80

Leu Leu Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys
85 90 95

Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Leu Ser Gly Phe
100 105 110

Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
115 120 125

Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
130 135 140

Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Leu
145 150 155 160

Ala Ile Leu Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp
165 170 175

Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu
180 185 190

Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu
195 200 205

Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Thr Gly Ile Ile Lys
210 215 220

Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu
225 230 235 240

Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Thr Pro Tyr Asn
245 250 255

Leu Thr Ile Leu Ile Ser Val Phe Gln Asp Phe Leu Phe Thr His Glu
260 265 270

Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val
275 280 285

Ile Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Ala Phe Val
290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg Gln Leu Phe His Arg Arg Val
305 310 315 320

Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Leu
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Ala Gly Phe
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